Amendments to the Specification:

Please replace paragraph [0106] with the following amended paragraph:

--[0106] FIG. 2 (SEQ ID NO:4) provides the predicted amino acid sequence of the EGFRKD expressed protein used to obtain the crystals and structural coordinates of the present invention. Note that this amino acid sequence may comprise amino acids encoded by the ORF, as well as other amino acids encoded by the expression vector. Further information regarding sequence changes, if any, may be found in the examples.--

Please replace paragraph [0107] with the following amended paragraph:

--[0107] FIG. 3 (SEQ ID NOS:5-8) provides a sequence alignment of EGFRKD from various species. Homologs were identified with PSI-BLAST 2.2.2 using the March 16, 2003 version of the Genbank non-redundant database. DbClustal was used to create the multiple alignment. ESPript was used to generate the PostScript version of the alignment. The species is identified along with the Genbanki gi number (in parenthesis). The secondary structure of EGFRKD was calculated by STRIDE. References: Frishman, D; Argos, P. "STRIDE: Knowledge-based protein secondary structure assignment." Protein, 23:566-79, 1995; Thompson, J.D.; Plewniak, F; Thierry J; Poch O. "DbClustal: Rapid and reliable global multiple alignments of the protein sequences detected by database searches." Nucleic Acids Research, 28:2919-26, 2000; Gouet, P; Courcelle, E; Stuart DI; Metoz, F. "ESPript: analysis of multiple sequence alignments in PostScript." Bioinformatics, 15:305-08, 1999). Active site residues are indicated by a blackened oval.--

Please replace paragraph [0293] with the following amended paragraph:

--[0293] Human liver cDNA was synthesized using a standard cDNA synthesis kit following the manufacturers' instructions. The template for the cDNA synthesis was mRNA isolated from Hep G2 cells [ATCC HB-8065] using a standard RNA isolation kit. An open-reading frame for EGFRKD was amplified from the human liver cDNA by the polymerase chain reaction (PCR) using the following primers:

Forward primer: GCTCCCAACCAAGCTCTC (SEQ ID NO: 1)

Reverse primer: CCCCCTGAATGACAAGGTAG (SEQ ID NO: 2)--

Please replace paragraph [0294] with the following amended paragraph:

--[0294] The PCR product (858 base pairs expected) was electrophoresed on a 1.2% E-gel (Cat. #G5018-01), Invitrogen Corporation) and the appropriate size band was excised from the gel and eluted using a standard gel extraction kit. The eluted DNA was TOPO ligated into a GATEWAY™ (Invitrogen Corporation) adapted pcDNA6 AttB HisC vector which was custom TOPO adapted by Invitrogen Corporation. The resulting sequence of the gene after being TOPO ligated into the vector, from the start sequence through the stop site was as follows: ATGGCCCTT 3' [EGFRKD]5' AAGGGCATCATCACCATCACCACTGA (SEQ ID NO:3). The EGFRKD expressed using this vector has an N-terminal methionine, the kinase domain of EGFRKD, and a C terminal 6 X His-tag. Figure 6.--